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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=25; hr=17; min=43; sec=12; ms=958;]

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Reviewer Comments:

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING
BRAIN/NERVE CELL PROTECTIVE AGENT

The above <120> response exceeds the Sequence Rules' required 72-character limit per line (this includes white spaces). Please insert a hard return after "SCREENING."

<210> 5

<211> 291

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(291)

<223>

<220>

<221> sig_peptide

<222> (1)..(81)

<223>

<220>

<221> mat_peptide

<222> (82)..()

<223>

<400> 5

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Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val	
-25 -20 -15	
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac	96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp	
-10 -5 -1 1 5	
tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg	144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
ggt ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc	192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag	240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag	288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
atg	291
Met	

70

In the above last line, "70" is not properly aligned under "Met," the last amino acid. Same type of error in Sequence 7.

Application No: 10547532 Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
E 201	Mandatory field data missing in <223> in SEQ ID (5)
W 112	Upper case found in data; Found at position(291) SeqId(5)
E 259	Found undefined lettercode; POS (293) SEQID(5)
E 254	The total number of bases conflicts with running total, Input: 70, Calculated : 294 SEQID(5)
E 253	The number of bases differs from <211> Input: 291 Calculated:294
E 201	Mandatory field data missing in <223> in SEQ ID (7)
W 112	Upper case found in data; Found at position(1122) SeqId(7)
E 259	Found undefined lettercode; POS (1124) SEQID(7)
W 112	Upper case found in data; Found at position(1125) SeqId(7)
E 259	Found undefined lettercode; POS (1127) SEQID(7)
W 112	Upper case found in data; Found at position(1128) SeqId(7)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
E 259	Found undefined lettercode; POS (1130) SEQID(7)
W 112	Upper case found in data; Found at position(1131) SeqId(7)
E 259	Found undefined lettercode; POS (1134) SEQID(7)
W 112	Upper case found in data; Found at position(1134) SeqId(7)
W 112	Upper case found in data; Found at position(1137) SeqId(7)
E 259	Found undefined lettercode; POS (1139) SEQID(7)
E 254	The total number of bases conflicts with running total, Input: 370, Calculated : 1140 SEQID(7)
E 253	The number of bases differs from <211> Input: 1122
E 201	Mandatory field data missing in <223> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
E 201	Mandatory field data missing in <223> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

Input Set:

Output Set:

Started: 2008-01-17 13:20:25.407
Finished: 2008-01-17 13:20:35.219
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 812 ms
Total Warnings: 17
Total Errors: 25
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10547532

<141> 2008-01-17

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

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<222> (1)..(78)

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<222> (79)..()

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Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu

-25

-20

-15

cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc 96

Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys

-10

-5

-1

1

5

tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc 144

Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly

10

15

20

ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc 192

Phe	Thr	Arg	Gln	Leu	Ala	Asn	Glu	Gly	Cys	Asp	Ile	Asn	Ala	Ile	Ile		
	25						30					35					
ttt	cac	aca	aag	aaa	aag	ttg	tct	gtg	tgc	gca	aat	cca	aaa	cag	act	240	
Phe	His	Thr	Lys	Lys	Lys	Leu	Ser	Val	Cys	Ala	Asn	Pro	Lys	Gln	Thr		
	40					45					50						
tgg	gtg	aaa	tat	att	gtg	cgt	ctc	ctc	agt	aaa	aaa	gtc	aag	aac	atg	288	
Trp	Val	Lys	Tyr	Ile	Val	Arg	Leu	Leu	Ser	Lys	Lys	Val	Lys	Asn	Met		
55					60					65					70		

<210> 2
 <211> 96
 <212> PRT
 <213> Homo sapiens

Met	Cys	Cys	Thr	Lys	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Met	Ser	Val	Leu		
	-25					-20					-15						
Leu	Leu	His	Leu	Cys	Gly	Glu	Ser	Glu	Ala	Ala	Ser	Asn	Phe	Asp	Cys		
-10					-5				-1	1				5			
Cys	Leu	Gly	Tyr	Thr	Asp	Arg	Ile	Leu	His	Pro	Lys	Phe	Ile	Val	Gly		
			10					15					20				
Phe	Thr	Arg	Gln	Leu	Ala	Asn	Glu	Gly	Cys	Asp	Ile	Asn	Ala	Ile	Ile		
	25					30					35						
Phe	His	Thr	Lys	Lys	Lys	Leu	Ser	Val	Cys	Ala	Asn	Pro	Lys	Gln	Thr		
	40					45					50						
Trp	Val	Lys	Tyr	Ile	Val	Arg	Leu	Leu	Ser	Lys	Lys	Val	Lys	Asn	Met		
55					60					65					70		

<210> 3
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 <212> DNA
 <213> Rattus norvegicus

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 <223>

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-25					-20					-15				-10			
gct	tac	ctc	tgc	agc	cag	tca	gaa	gca	gca	agc	aac	ttt	gac	tgc	tgc	96	
Ala	Tyr	Leu	Cys	Ser	Gln	Ser	Glu	Ala	Ala	Ser	Asn	Phe	Asp	Cys	Cys		
				-5				-1	1				5				
ctc	acg	tac	aca	aag	aac	gtg	tat	cat	cat	gcg	aga	aat	ttt	gtg	ggt	144	
Leu	Thr	Tyr	Thr	Lys	Asn	Val	Tyr	His	His	Ala	Arg	Asn	Phe	Val	Gly		

10	15	20	
ttc aca aca cag atg gcc gac gaa gct tgt gac att aat gct atc atc			192
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile			
25	30	35	
ttt cac ctg aag tcg aaa aga tcc gtg tgc gct gac cca aag cag atc			240
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile			
40	45	50	55
tgg gtg aaa agg att ttg cac ctc ctc agc cta aga acc aag aag atg			288
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met			
60	65	70	

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 <212> PRT
 <213> Rattus norvegicus

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-5	-1 1 5
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly	
10	15 20
Phe Thr Thr Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile Ile	
25	30 35
Phe His Leu Lys Ser Lys Arg Ser Val Cys Ala Asp Pro Lys Gln Ile	
40	45 50 55
Trp Val Lys Arg Ile Leu His Leu Leu Ser Leu Arg Thr Lys Lys Met	
60	65 70

<210> 5
 <211> 291
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(291)
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<220>
 <221> sig_peptide
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 <221> mat_peptide
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Met Ala Cys Gly Gly Lys Arg Leu Leu Phe Leu Ala Leu Ala Trp Val	
-25	-20 -15
ctg ctg gct cac ctc tgc agc cag gca gaa gca gca agc aac tac gac	96
Leu Leu Ala His Leu Cys Ser Gln Ala Glu Ala Ala Ser Asn Tyr Asp	
-10	-5 -1 1 5

tgt tgc ctc tcg tac ata cag acg cct ctt cct tcc aga gct att gtg	144
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
ggg ttc aca aga cag atg gcc gat gaa gct tgt gac att aat gct atc	192
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
atc ttt cac acg aag aaa aga aaa tct gtg tgc gct gat cca aag cag	240
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
aac tgg gtg aaa agg gct gtg aac ctc ctc agc cta aga gtc aag aag	288
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
atg	291
Met	70

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-10 -5 -1 1 5	
Cys Cys Leu Ser Tyr Ile Gln Thr Pro Leu Pro Ser Arg Ala Ile Val	
10 15 20	
Gly Phe Thr Arg Gln Met Ala Asp Glu Ala Cys Asp Ile Asn Ala Ile	
25 30 35	
Ile Phe His Thr Lys Lys Arg Lys Ser Val Cys Ala Asp Pro Lys Gln	
40 45 50	
Asn Trp Val Lys Arg Ala Val Asn Leu Leu Ser Leu Arg Val Lys Lys	
55 60 65	
Met	
70	

<210> 7
 <211> 1122
 <212> DNA
 <213> Homo sapiens

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gat tat ttt gtg tca gtc aat act tca tat tac tca gtt gat tct gag	96
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu	
20 25 30	
atg tta ctg tgc tcc ttg cag gag gtc agg cag ttc tcc agg cta ttt	144
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe	
35 40 45	

gta ccg att gcc tac tcc ttg atc tgt gtc ttt ggc ctc ctg ggg aat	192
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn	
50 55 60	
att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg	240
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met	
65 70 75 80	
aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt	288
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val	
85 90 95	
ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt	336
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val	
100 105 110	
ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac	384
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn	
115 120 125	
ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac	432
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr	
130 135 140	
atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca	480
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr	
145 150 155 160	
cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc	528
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val	
165 170 175	
atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa	576
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln	
180 185 190	
ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc	624
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile	
195 200 205	
agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt	672
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe	
210 215 220	
atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc	720
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr	
225 230 235 240	
ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc	768
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile	
245 250 255	
ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg	816
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met	
260 265 270	
gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc	864
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys	
275 280 285	
cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg	912
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu	
290 295 300	
gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg	960
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly	
305 310 315 320	
cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt	1008
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys	
325 330 335	
gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac	1056
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr	
340 345 350	

tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac aat	1104
Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn	
355 360 365	
gcg tcg tcc ttc act atg	1122
Ala Ser Ser Phe Thr Met	370

<210> 8
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 8

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Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe	
35 40 45	
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn	
50 55 60	
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met	
65 70 75 80	
Thr Asp Val Tyr Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val	
85 90 95	
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val	
100 105 110	
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn	
115 120 125	
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr	
130 135 140	
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr	
145 150 155 160	
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val	
165 170 175	
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln	
180 185 190	
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile	
195 200 205	
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Gly Phe Phe	
210 215 220	
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr	
225 230 235 240	
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile	
245 250 255	
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met	
260 265 270	
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys	
275 280 285	
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu	
290 295 300	
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly	
305 310 315 320	
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys	
325 330 335	
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr	
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Ala Ser Ser Phe Thr Met
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<222> (1)..(1101)
<223>

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Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
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gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata 144
Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
35 40 45
tgt gtc ttt ggc ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc 192
Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
50 55 60
ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg 240
Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
65 70 75 80
gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288
Ala Ile Thr